In the Claims:

Claim 1 (Canceled).

2. (Previously presented): A method for synthesizing a double stranded nucleic acid molecule comprising:

(a) mixing one or more nucleic acid templates with a polypeptide having polymerase activity and one or more primers comprising at least a first recombination site or portions thereof;

(b) incubating said mixture under conditions sufficient to synthesize a first nucleic acid molecule which is complementary to all or a portion of said one or more templates and which comprises at least said first recombination site or portions thereof; and

(c) incubating said first nucleic acid molecule in the presence of one or more primers comprising at least a second recombination site or portions thereof under conditions sufficient to synthesize a second nucleic acid molecule complementary to all or a portion of said first nucleic acid molecule, thereby producing a double stranded nucleic acid molecule comprising at least said first and second recombination sites or portions thereof,

wherein at least one of said first and second recombination sites comprises one or more mutations that remove one or more stop codons from said recombination sites.

3. (Previously presented): A method for synthesizing a double stranded nucleic acid molecule comprising:

(a) mixing one or more nucleic acid templates with a polypeptide having polymerase activity and one or more primers comprising at least a first recombination site or portions thereof;

(b) incubating said mixture under conditions sufficient to synthesize a first nucleic acid molecule which is complementary to all or a portion of said one or more templates and which comprises at least said first recombination site or portions thereof; and

(c) incubating said first nucleic acid molecule in the presence of one or more primers comprising at least a second recombination site or portions thereof under conditions sufficient to synthesize a second nucleic acid molecule complementary to all or a portion of said first nucleic acid molecule, thereby producing a double stranded nucleic acid molecule comprising at least said first and second recombination sites or portions thereof,

wherein at least one of said first and second recombination sites comprises one or more mutations that avoids hairpin formation in said recombination sites.

4. (Previously presented): A method for synthesizing a double stranded nucleic acid molecule comprising:

(a) mixing one or more nucleic acid templates with a polypeptide having polymerase activity and one or more primers comprising at least a first recombination site or portions thereof;

(b) incubating said mixture under conditions sufficient to synthesize a first nucleic acid molecule which is complementary to all or a portion of said one or more templates and which comprises at least said first recombination site or portions thereof; and

(c) incubating said first nucleic acid molecule in the presence of one or more primers comprising at least a second recombination site or portions thereof under conditions sufficient to synthesize a second nucleic acid molecule complementary to all or a portion of said first nucleic acid molecule, thereby producing a double stranded nucleic acid molecule comprising at least said first and second recombination sites or portions thereof,

wherein at least one of said first and second recombination sites comprises at least one nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-16 or a DNA sequence complementary thereto.

5. (Previously presented): The method of claim 2, wherein said recombination sites or portions thereof are located at or near one terminus of said double stranded nucleic acid molecule.

6. (Previously presented): The method of claim 3, wherein said recombination sites or portions thereof are located at or near one terminus of said double stranded nucleic acid molecule.

7. (Previously presented): The method of claim 4, wherein said recombination sites or portions thereof are located at or near one terminus of said double stranded nucleic acid molecule.

8. (Previously presented): The method of claim 2, wherein said first or second recombination sites are selected from the group consisting of *att*B sites, *att*P sites, *att*L sites, *att*R sites, *lox* sites, and portions thereof.

9. (Previously presented): The method of claim 3, wherein said first or second recombination sites are selected from the group consisting of *att*B sites, *att*P sites, *att*L sites, *att*R sites, *lox* sites, and portions thereof.

10. (Previously presented): The method of claim 4, wherein said first or second recombination sites are selected from the group consisting of *att*B sites, *att*P sites, *att*L sites, *att*R sites, *lox* sites, and portions thereof.

11. (Previously presented): The method of claim 2, further comprising amplifying said first and second nucleic acid molecules.

12. (Previously presented): The method of claim 3, further comprising amplifying said first and second nucleic acid molecules.

13. (Previously presented): The method of claim 4, further comprising amplifying said first and second nucleic acid molecules.

14. (Previously presented): The method of claim 2, wherein said recombination sites or portions thereof are located at or near one or both termini of said double stranded nucleic acid molecule.

15. (Previously presented): The method of claim 3, wherein said recombination sites or portions thereof are located at or near one or both termini of said double stranded nucleic acid molecule.

16. (Previously presented): The method of claim 4, wherein said recombination sites or portions thereof are located at or near one or both termini of said double stranded nucleic acid molecule.

17. (Previously presented): The method of claim 2, wherein said first and second recombination sites do not recombine with each other.

18. (Previously presented): The method of claim 3, wherein said first and second recombination sites do not recombine with each other.

19. (Previously presented): The method of claim 4, wherein said first and second recombination sites do not recombine with each other.

20. (Previously presented): A method for synthesizing a double stranded nucleic acid molecule comprising:

(a) mixing one or more nucleic acid templates with a polypeptide having polymerase activity and one or more primers comprising at least a first recombination site or portions thereof;

(b) incubating said mixture under conditions sufficient to synthesize a first nucleic acid molecule which is complementary to all or a portion of said one or more templates and which comprises at least said first recombination site or portions thereof; and

(c) incubating said first nucleic acid molecule in the presence of one or more primers comprising at least a second recombination site or portions thereof under conditions sufficient to synthesize a second nucleic acid molecule complementary to all or a portion of said first nucleic acid molecule, thereby producing a double stranded nucleic acid molecule comprising at least said first and second recombination sites or portions thereof,

wherein at least one of said first and second recombination sites comprises at least one nucleotide sequence that has at least 80-99% homology to a nucleotide

sequence selected from the group of sequences consisting of SEQ ID NOs: 39-43, and a corresponding or complementary DNA or RNA sequence.

21. (Previously presented): A method for synthesizing a double stranded nucleic acid molecule comprising:

(a) mixing one or more nucleic acid templates with a polypeptide having polymerase activity and one or more primers comprising at least a first recombination site or portions thereof;

(b) incubating said mixture under conditions sufficient to synthesize a first nucleic acid molecule which is complementary to all or a portion of said one or more templates and which comprises at least said first recombination site or portions thereof; and

(c) incubating said first nucleic acid molecule in the presence of one or more primers comprising at least a second recombination site or portions thereof under conditions sufficient to synthesize a second nucleic acid molecule complementary to all or a portion of said first nucleic acid molecule, thereby producing a double stranded nucleic acid molecule comprising at least said first and second recombination sites or portions thereof,

wherein at least one of said first and second recombination sites comprises at least one nucleotide sequence that has at least 80-99% homology to a nucleotide

sequence selected from the group of sequences consisting of SEQ ID NOs: 1-16, and a corresponding or complementary DNA or RNA sequence.

22. (Previously presented): The method of claim 20, wherein said recombination sites or portions thereof are located at or near one terminus of said double stranded nucleic acid molecule.

23. (Previously presented): The method of claim 21, wherein said recombination sites or portions thereof are located at or near one terminus of said double stranded nucleic acid molecule.

24. (Previously presented): The method of claim 20, further comprising amplifying said first and second nucleic acid molecules.

25. (Previously presented): The method of claim 21, further comprising amplifying said first and second nucleic acid molecules.

26. (Previously presented): The method of claim 20, wherein said recombination sites or portions thereof are located at or near one or both termini of said double stranded nucleic acid molecule.

27. (Previously presented): The method of claim 21, wherein said recombination sites or portions thereof are located at or near one or both termini of said double stranded nucleic acid molecule.

28. (Previously presented): The method of claim 20, wherein said first and second recombination sites do not recombine with each other.

29. (Previously presented): The method of claim 21, wherein said first and second recombination sites do not recombine with each other.